sequences which is a portion of a sequence neighboring the junction between sequence elements. Additionally, Applicant has amended the claims to recite a nucleic acid probe array comprising a set of probes to interrogate the joining sequence. Applicant respectfully submits that Cronin does not teach every element of the amended claims. Therefore, this rejection under 35 U.S.C. 102(b) should be withdrawn.

Anticipation Rejection Under 35 U.S.C. § 102(e)

The Examiner has rejected Claims 1-2 under 35 U.S.C. 102(e) as being anticipated by Hacia *et. al.* (U.S. Patent No. 6,342,355). Applicants respectfully traverse the rejection.

Hacia teaches an array one probe set with probes that tile a region of interest in a reference allele. In contrast, Applicant's invention teaches a nucleic acid probe array comprising a set of probes to interrogate the joining sequence between two sequence elements (such as two exons). Applicant respectfully submits that the Examiner has failed to show that Hacia teaches every element of the amended claims. Therefore, this rejection under 35 U.S.C. 102(e) should be withdrawn.

Obviousness Rejection under 35 U.S.C. § 103(a)

The Examiner has rejected Claims 4-10 as being rejected under 35 U.S.C. 103(a) as being unpatentable over Cronin *et al.* in view of Hacia *et al.* and further in view of Lockhart *et al.* Applicants respectfully disagree with the Examiner.

Both Cronin *et al.* and Hacia teach the detection of sequence variations using microarrays. Lockhart teaches high density probe arrays technology. However, the amended claims are directed to the identification of sequence junctions (such as junctions between exons). Applicants respectfully submit that the Examiner has not shown that the cited references provide suggestions or motivations for the claimed invention. Therefore, this rejection of claims should be withdrawn.

CONCLUSION

For these reasons, Applicant believes all pending claims are now in condition for allowance and should be passed to issue. If the Examiner feels that a telephone conference would in any way expedite the prosecution of the application, please do not hesitate to call the undersigned at (408) 731-5699.

The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account 01-0431.

If the Examiner has any questions pertaining to this application, the Examiner is requested to contact the undersigned attorney.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE TO THE APPLICATION

In the Specification

Please amend the first paragraph on page 4 as follows:

In one aspect of the invention, a nucleic acid probe array comprising a set of probes [for interrogating] to interrogate the joining sequence between a first sequence element and a second sequence element is provided. In some embodiments, the probes on the probe array are oligonucleotides. The first sequence element may be a first exon and the second sequence element may be a second exon. The joining sequence is the portion of the sequence neighboring the junction between the first and second sequence. If the sequence elements are exons, the joining sequence is the 3' sequence of one exon and 5' sequence of another exon. The joining sequence should be at least 20 bases in length, preferably at least 30 bases in length, more preferably at least 40 bases in length, even more preferably at least 50 bases and most preferably 100 bases in length.

In the Claims

Please amend Claim 1 as follows:

1. (amended) A nucleic acid probe array comprising a set of probes [for interrogating] to interrogate the joining sequence between a first sequence element and a second sequence element.